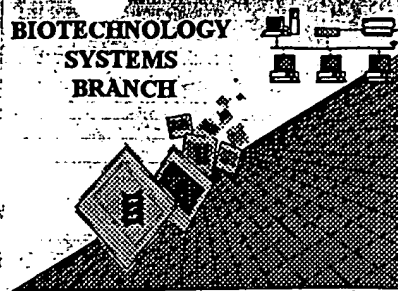


BEST AVAILABLE COPY

## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



STIC MAIL ROOM

Aug - 8 2000

RECEIVED

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/509,449

Source:

1643

Date Processed by STIC:

7/24/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/509449

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2      Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3      Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4      Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5      Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6      Variable Length      Sequence(s)      contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7      PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)     . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8      Skipped Sequences      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9      Skipped Sequences      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
<400> sequence id number  
000
- 10      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11      Use of <213>Organism      Sequence(s)      are missing this mandatory field or its response.  
(NEW RULES)      3, 4, 5, 6, 9
- 12      Use of <220>Feature      Sequence(s)      are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13      PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1643

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/509,449

DATE: 07/24/2000  
TIME: 13:38:40

Input Set : A:\PTO.txt  
Output Set: N:\CRF3\07242000\I509449.raw

*Suggestion: Consult  
new sequence  
Does Not Comply  
Corrected Diskette Needed*

3 <110> APPLICANT: Tonen Corporation  
5 <120> TITLE OF INVENTION: Method for Measurement of hepatitis C virus  
7 <130> FILE REFERENCE: G902  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/509,449  
C--> 9 <141> CURRENT FILING DATE: 2000-03-28  
9 <150> PRIOR APPLICATION NUMBER: JP-10-216094  
10 <151> PRIOR FILING DATE: 1998-07-30  
E--> 12 <160> NUMBER OF SEQ ID NOS: 9

*See item 5  
on Enva  
summary  
sheet*

## ERRORED SEQUENCES

111 <210> SEQ ID NO: 6  
112 <211> LENGTH: 20  
113 <212> TYPE: PRT  
114 <213> ORGANISM: Artificial Sequence  
116 <220> FEATURE:  
E--> 118 <230> *22307 is an invalid numerical identifier.*  
W--> 120 <400> SEQUENCE: 6  
E--> 121 Asp Pro Arg His Arg Ser Arg Asn Val Gly Lys Val Leu Asp Thr Leu  
122 1 5 10 15  
123 Thr Cys Gly Phe  
124 20  
126 <210> SEQ ID NO: 7  
127 <211> LENGTH: 24  
128 <212> TYPE: DNA  
129 <213> ORGANISM: Artificial Sequence  
W--> 131 <220> FEATURE: Probe  
E--> 133 <230> Synthetic DNA  
W--> 135 <223> OTHER INFORMATION:  
135 <400> SEQUENCE: 7  
136 gaattcatgg gcacgaatcc taaa  
138 <210> SEQ ID NO: 8  
139 <211> LENGTH: 21  
140 <212> TYPE: DNA  
141 <213> ORGANISM: Artificial Sequence  
W--> 143 <220> FEATURE: Probe  
E--> 145 <230> Synthetic DNA  
W--> 147 <223> OTHER INFORMATION:  
147 <400> SEQUENCE: 8  
148 ttagtctctcc agaaccgga c  
150 <210> SEQ ID NO: 9  
151 <211> LENGTH: 16  
152 <212> TYPE: PRT  
153 <213> ORGANISM: Artificial Sequence  
155 <220> FEATURE:

*see item 12 on Enva  
summary*

*Use <2237  
when explaining  
source material  
of Artificial  
Sequence*

*<2207 does not have a  
response. It is a "leader" only.*

*Insert all  
explanations of  
source material  
on same line as <2237.*

*same Enva*

*see item 12 on Enva summary sheet*

RECEIVED  
JUL-8 2000  
TC 1000 MAIL ROOM

## RAW SEQUENCE LISTING

DATE: 07/24/2000

PATENT APPLICATION: US/09/509,449

TIME: 13:38:40

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07242000\I509449.raw

E--> 157 ~~<230>~~ *delete*  
 W--> 159 <223> OTHER INFORMATION: *insert explanation of source material*  
 159 <400> SEQUENCE: 9  
 160 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile  
 161 1 5 10 15  
 163 <210> SEQ ID NO: 10  
 164 <211> LENGTH: 1197  
 165 <212> TYPE: DNA  
 166 <213> ORGANISM: Artificial Sequence  
 168 <220> FEATURE: *replace with <223>*  
 E--> 170 ~~<230>~~ Nucleotide sequence coding for chimeric antigen  
 W--> ~~172 <223> OTHER INFORMATION:~~  
 172 <400> SEQUENCE: 10  
 173 gaa ttc acc aaa gtg ccg gtt gct tat gcg gcc aaa ggt tat aag gtc 48  
 174 Glu Phe Thr Lys Val Pro Val Ala Tyr Ala Ala Lys Gly Tyr Lys Val  
 175 5 10 15  
 176 ctg gtt ctg gac ccg agc gtt gcc agc acc ctg ggt ttc ggc gcg tat 96  
 177 Leu Val Leu Asp Pro Ser Val Ala Ser Thr Leu Gly Phe Gly Ala Tyr  
 178 20 25 30  
 179 ctg agc aag gcc cat ggt gtg aac ccg aac atc cgc acg ggc atc cgt 144  
 180 Leu Ser Lys Ala His Gly Val Asn Pro Asn Ile Arg Thr Gly Ile Arg  
 181 35 40 45  
 182 acc gtt acc acc ggt gct ccg gtg acc tat tcc acc tac ggt aaa tac 192  
 183 Thr Val Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Tyr  
 184 50 55 60  
 185 ctg gcg gac ggc ggt tgc gcc gcc ggt gcg tac gat gtg atc gga tct 240  
 186 Leu Ala Asp Gly Gly Cys Ala Gly Gly Ala Tyr Asp Val Ile Gly Ser  
 187 65 70 75 80  
 188 gga gag gag gtg gcc ctg tct aac act gga gag gtc ccc ttc tat ggc 288  
 189 Gly Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Val Pro Phe Tyr Gly  
 190 85 90 95  
 191 cgc gcg atc ccg atc gaa gcg atc aaa gcc ggt cgc cat ctg gtt ttc 336  
 192 Arg Ala Ile Pro Ile Glu Ala Ile Lys Gly Gly Arg His Leu Val Phe  
 193 100 105 110  
 194 tgc cat agc aag gag aaa tgc gat gaa ctg gcg agc gcg ctg tcc gga 384  
 195 Cys His Ser Lys Glu Lys Cys Asp Glu Leu Ala Ser Ala Leu Ser Gly  
 196 115 120 125  
 197 ttg ggt ctg aac gct gtg gca ttc tat cgc ggt ctg gac gtg agc att 432  
 198 Leu Gly Leu Asn Ala Val Ala Phe Tyr Arg Gly Leu Asp Val Ser Ile  
 199 130 135 140  
 200 atc ccg acc cag gcc gat gtg gtt atc gtt agc acc gat gcg ctg atg 480  
 201 Ile Pro Thr Gln Gly Asp Val Val Ile Val Ser Thr Asp Ala Leu Met  
 202 145 150 155 160  
 203 acc ggt ttt acc gcc gat ttt gac tca gtg gtc gac tgt aac aca tgc 528  
 204 Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Val Asp Cys Asn Thr Cys  
 205 165 170 175  
 206 atc acc cag gga tct gga ctg gta agc ttc gcg agc cat gtg ccg tac 576  
 207 Ile Thr Gln Gly Ser Gly Leu Val Ser Phe Ala Ser His Val Pro Tyr  
 208 180 185 190

*ignore*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/509,449

DATE: 07/24/2000

TIME: 13:38:40

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07242000\I509449.raw

```

209 atc gag cag ggt atg caa ctg agc gaa caa ttt aag cag aag agc ctg      624
210 ile Glu Gln Gly Met Gln Leu Ser200Glu Gln Phe Lys Gln Lys Ser Leu      205
211      195
212 ggt ctg ctg cag acc gcg acc aaa cag gcg gag gcg gcc gcc ccg gtg      672
213 Gly Leu Leu Gln Thr Ala Thr Lys Gln Ala Glu Ala Ala Ala Pro Val      220
214      210
215 gtt ggc acc ccg aaa agc cgc cgt ccg gaa ggt cgt gcc tgg gcg caa      720
216 Val Gly Thr Pro Lys Ser Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln      240
217 225      230
218 ccg ggt acc atc atc ctg agc ggt cgt ccg gcg gtt gta ccg gat cgt      768
219 Pro Gly Thr Ile Ile Leu Ser Gly Arg Pro Ala Val Val Pro Asp Arg      255
220      245
221 gaa gtg ctg tat caa gaa ttt ctc gag gcc tct aga gcg gct ctc att      816
222 Glu Val Leu Tyr Gln Glu Phe Leu Glu Ala Ser Arg Ala Ala Leu Ile      270
223      260
224 gaa gag ggg caa ccg ata gcc gag atg ctg aag tcc aag atc cag ggc      864
225 Glu Glu Gly Gln Arg Ile Ala Glu Met Leu Lys Ser Lys Ile Gln Gly      285
226      275
227 tta ctg cag caa gcc tcc aag cag gcc caa gac ata aaa atc gac ggt      912
228 Leu Leu Gln Gln Ala Ser Lys Gln Ala Gln Asp Ile Lys Ile Asp Gly      300
229      290
230 acc ctg att att ccg aaa gat cgt cgc agc acc ggt aaa agc tgg ggt      960
231 Thr Leu Ile Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly      315
232 305      310
233 aaa ccg ggc ttc ctc atc gat agc ttg cat atc aac cag cga gcc gtc      1008
234 Lys Pro Gly Phe Leu Ile Asp Ser Leu His Ile Asn Gln Arg Ala Val      335
235      325
236 gtt gca ccg gac aag gag gtc ctt tat gag gct ttt gat gag atg gag      1056
237 Val Ala Pro Asp Lys Glu Val Leu Tyr Glu Ala Phe Asp Glu Met Glu      350
238      340
239 ctc gcc atg ggc acc aac ccg aaa ccg gag cgt aaa agc aag cgt aac      1104
240 Leu Ala Met Gly Thr Asn Pro Lys Pro Glu Arg Lys Ser Lys Arg Asn      365
241      355
242 acc aac cgt aaa ccg cag gat att aaa ttc ccg ggt agt ggt cag gtg      1152
243 Thr Asn Arg Lys Pro Gln Asp Ile Lys Phe Pro Gly Ser Gly Gln Val      380
244      370
245 gtg ggt ggt gtg tac ctg gtg ccg cgt cgt ggt ccg taaggatcc      1197
246 Val Gly Gly Val Tyr Leu Val Pro Arg Arg Gly Pro      395
247 385      390
249 <210> SEQ ID NO: 11
250 <211> LENGTH: 396
251 <212> TYPE: PRT
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
E--> 256 (230) Amino acid sequence of chimeric antigen
W--> 258 <225> OTHER INFORMATION:
258 <400> SEQUENCE: 11
259 Glu Phe Thr Lys Val Pro Val Ala Tyr Ala Ala Lys Gly Tyr Lys Val
260      5      10      15

```

*last sequence in file**same error**(see next page)*

## RAW SEQUENCE LISTING

DATE: 07/24/2000

PATENT APPLICATION: US/09/509,449

TIME: 13:38:40

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07242000\I509449.raw

```

261 Leu Val Leu Asp Pro Ser Val Ala Ser Thr Leu Gly Phe Gly Ala Tyr
262          20          25          30
263 Leu Ser Lys Ala His Gly Val Asn Pro Asn Ile Arg Thr Gly Ile Arg
264          35          40          45
265 Thr Val Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Tyr
266          50          55          60
267 Leu Ala Asp Gly Gly Cys Ala Gly Gly Ala Tyr Asp Val Ile Gly Ser
268 65          70          75          80
269 Gly Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Val Pro Phe Tyr Gly
270          85          90          95
271 Arg Ala Ile Pro Ile Glu Ala Ile Lys Gly Gly Arg His Leu Val Phe
272          100         105         110
273 Cys His Ser Lys Glu Lys Cys Asp Glu Leu Ala Ser Ala Leu Ser Gly
274          115         120         125
275 Leu Gly Leu Asn Ala Val Ala Phe Tyr Arg Gly Leu Asp Val Ser Ile
276          130         135         140
277 Ile Pro Thr Gln Gly Asp Val Val Ile Val Ser Thr Asp Ala Leu Met
278 145          150         155         160
279 Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Val Asp Cys Asn Thr Cys
280          165         170         175
281 Ile Thr Gln Gly Ser Gly Leu Val Ser Phe Ala Ser His Val Pro Tyr
282          180         185         190
283 Ile Glu Gln Gly Met Gln Leu Ser Glu Gln Phe Lys Gln Lys Ser Leu
284          195         200         205
285 Gly Leu Leu Gln Thr Ala Thr Lys Gln Ala Glu Ala Ala Pro Val
286          210         215         220
287 Val Gly Thr Pro Lys Ser Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln
288 225          230         235         240
289 Pro Gly Thr Ile Ile Leu Ser Gly Arg Pro Ala Val Val Pro Asp Arg
290          245         250         255
291 Glu Val Leu Tyr Gln Glu Phe Leu Glu Ala Ser Arg Ala Ala Leu Ile
292          260         265         270
293 Glu Glu Gly Gln Arg Ile Ala Glu Met Leu Lys Ser Lys Ile Gln Gly
294          275         280         285
295 Leu Leu Gln Gln Ala Ser Lys Gln Ala Gln Asp Ile Lys Ile Asp Gly
296          290         295         300
297 Thr Leu Ile Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly
298 305          310         315         320
299 Lys Pro Gly Phe Leu Ile Asp Ser Leu His Ile Asn Gln Arg Ala Val
300          325         330         335
301 Val Ala Pro Asp Lys Glu Val Leu Tyr Glu Ala Phe Asp Glu Met Glu
302          340         345         350
303 Leu Ala Met Gly Thr Asn Pro Lys Pro Glu Arg Lys Ser Lys Arg Asn
304          355         360         365
305 Thr Asn Arg Lys Pro Gln Asp Ile Lys Phe Pro Gly Ser Gly Gln Val
306          370         375         380
307 Val Gly Gly Val Tyr Leu Val Pro Arg Arg Gly Pro
308 385          390         395
309 179

```

delite

See next page

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/509,449

DATE: 07/24/2000

TIME: 13:38:41

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07242000\I509449.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
 L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:118 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
 L:120 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:121 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
 L:131 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
 L:133 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
 L:135 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:143 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
 L:145 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
 L:147 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:157 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
 L:159 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:170 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
 L:172 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:256 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
 L:258 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:12 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (9) Counted (11)